

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 13:59:32 ; Search time 39 Seconds
(Without alignments)
54.230 Million cell updates/sec

Title: US-09-914-213-2

Perfect score: 116

Sequence: 1 GLEISERINEDIKECFDDME 22

Scoring table: BIOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	1480	1 DVHUCF	cystic fibrosis tr
2	106	91.4	1481	1 A39323	cystic fibrosis tr
3	103	88.8	1450	2 JC6139	cystic fibrosis tr
4	94	81.0	1485	2 S23756	CFTR protein - Afr
5	87	75.0	1476	1 A39901	cystic fibrosis tr
6	87	75.0	1476	1 A40303	cystic fibrosis tr
7	87	75.0	1492	2 A39322	cystic fibrosis tr
8	57	49.1	378	2 A32916	long-chain-fatty-a
9	51	44.0	705	2 H89900	translation initia
10	50	43.1	631	2 S67268	hypothetical prote
11	49	42.2	257	2 A28664	enterotoxin A prec
12	49	42.2	257	2 A28179	coproporphyrinogen
13	49	42.2	457	2 A64603	phosphomannomutase
14	48.5	41.8	565	2 C69835	probable calmoduli
15	48	41.4	154	2 G85041	coenzyme F420-quin
16	48	41.4	410	2 E69478	oxygen-independent
17	48	41.4	457	2 H71911	GTP-MSV100 probabl
18	48	41.4	1087	2 T30330	GTP-binding membra
19	47.5	40.9	230	2 T28262	protein T25N20.11
20	47	40.5	603	2 S76959	phage-related repl
21	47	40.5	1048	2 C86189	probable ATP-depen
22	46.5	40.1	235	1 E69883	thioredoxin (limpor
23	46.5	40.1	265	2 D84643	conserved hypotet
24	46.5	40.1	380	2 T17423	probable heat choc
25	46	39.7	104	2 D86830	long-chain-fatty-a
26	46	39.7	232	2 C89938	corrinoid/Iron-sul
27	46	39.7	244	2 C96796	
28	46	39.7	373	2 S15161	
29	46	39.7	468	1 H64313	

ALIGNMENTS

RESULT 1

DVHUCF

Cystic fibrosis transmembrane conductance regulator - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1990 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A39069; A30300; A42805; S10943; S15354; S10951

R:Zielenski, J.; Rozmahel, R.; Bozon, D.; Kerem, B.; Grzelczak, Z.; Riordan, J.R.; Ro

Genomics 10, 214-228, 1991

A:Title: Genomic DNA sequence of the cystic fibrosis transmembrane conductance regula

A:Reference number: A39069; MUID:91257831; PMID:1710598

A:Accession: A39069

A:Molecule type: DNA

A:Residues: 1-1480 <ZIE>

A:Cross-references: GB:M55131; NID:9306536; PIDN:AAC13657.1; PID:9306538

R:Riordan, J.R.; Rommens, J.M.; Kerem, B.; Alon, N.; Rozmahel, R.; Grzelczak, Z.; Zie

Science 245, 1066-1073, 1999

A:Title: Identification of the cystic fibrosis gene: cloning and characterization of

A:Reference number: A30300; MUID:89368940; PMID:2475911

A:Accession: A30300

A:Molecule type: mRNA

A:Residues: 1-619, 'N', 621-832, 'L', 834-1149, 'I', 1151-1480 <RIO>

A:Cross-references: GB:M28668; NID:9180331

A:Note: This sequence has been revised in reference A39069

R:Ricciotto, M.R.; Cohn, J.A.; Bertuzzi, G.; Greengard, P.; Nairn, A.C.

J. Biol. Chem. 267, 12742-12752, 1992

A:Title: Phosphorylation of the cystic fibrosis transmembrane conductance regulator.

A:Reference number: A42805; MUID:92316961; PMID:1377674

A:Accession: A42805

A:Molecule type: protein

A:Residues: 682-690, 'E', 693-725, 'T', 727-743, 'T', 747-815 <PIC>

R:Cutting, G.R.; Kasch, L.M.; Rosensteel, B.J.; Zielenski, J.; Tsai, L.C.; Antonarak

Nature 346, 366-369, 1990

A:Title: A cluster of cystic fibrosis mutations in the first nucleotide-binding fold

A:Reference number: S10943; MUID:90326187; PMID:1695717

A:Accession: S10943

A:Molecule type: nucleic acid sequence not shown

A:Residues: 542-560; 1340-1358 <CUT>

A:Note: Four mutations between residues 549-559 were identified in CF patients

R:Toshimura, K.; Nakamura, H.; Trapnell, B.C.; Dalemans, W.; Pavlanti, A.; Lecocq, J.

J. Biol. Chem. 266, 9140-9144, 1991

A:Title: The cystic fibrosis gene has a 'housekeeping'-type promoter and is expressed

A:Reference number: I55354; MUID:91225019; PMID:1709163

A:Accession: I55354

A:Molecule type: DNA

A:Status: translated from GB/EMBL/DBJ

A:Residues: 1-17 <RES>

A:Cross-references: GB:M58478; NID:9180291; PIDN:AAA1992.1; PID:9180292

A:Note: neither the complete nucleic acid sequence nor the complete translation are s

C:Comment: This protein (CFTR) is directly responsible for cystic fibrosis (CF), a di

piratory tract. A single residue deletion (Phe-508) is detected in most CF patients;

30	46	39.7	515	2 C71158	probable thermosta
31	46	39.7	562	2 H88071	protein ZK1240.3 l
32	46	39.7	599	2 G83821	DNA primase dnag l
33	46	39.7	707	1 DNMS	nucleolin - mouse
34	46	39.7	1336	2 T23310	hypothetical prote
35	46	39.7	1882	1 GNVYR	genome polypeptide
36	45.5	39.2	1308	2 E71622	probable membrane
37	45	38.8	104	2 B69784	hypothetical prote
38	45	38.8	216	2 C88576	720G5.12 protein -
39	45	38.8	260	2 C70115	ribosomal protein
40	45	38.8	366	2 F71481	probable rod shape
41	45	38.8	366	2 D72027	cell shape-determi
42	45	38.8	366	2 H8596	rod shape protein-
43	45	38.8	366	2 E81742	cell shape-determi
44	45	38.8	593	2 A46733	Na+-transporting A
45	45	38.8	953	2 AH1972	hypothetical prote

uctance across the apical membrane of epithelial cells.

C:Genetics:
A:Gene: GDB:CFTR; CF
A:Cross-References: GDB:120584; OMIM:219700
A:Map position: 7q31.2-7q31.2
A:Introns: 18/2: 55/2: 91/3: 163/3: 193/3: 248/2: 290/2: 372/3: 403/3: 464/3: 528/3: 560
C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette
C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;
F:118-102/Domain: transmembrane #status predicted <TM1>
F:118-138/Domain: transmembrane #status predicted <TM2>
F:195-215/Domain: transmembrane #status predicted <TM3>
F:221-241/Domain: transmembrane #status predicted <TM4>
F:308-328/Domain: transmembrane #status predicted <TM5>
F:331-350/Domain: transmembrane #status predicted <TM6>
F:441-622/Domain: ATP-binding cassette homology <ABC1>
F:458-465/Region: nucleotide-binding motif A (P-loop)
F:568-572/Region: nucleotide-binding motif B
F:590-830/Region: R domain
F:860-880/Domain: transmembrane #status predicted <TM7>
F:912-932/Domain: transmembrane #status predicted <TM8>
F:991-1011/Domain: transmembrane #status predicted <TM9>
F:1103-1123/Domain: transmembrane #status predicted <TM10>
F:1123-1150/Domain: transmembrane #status predicted <TM11>
F:1227-1419/Domain: ATP-binding cassette homology <ABC2>
F:1244-1251/Region: nucleotide-binding motif A (P-loop)
F:1366-1370/Region: nucleotide-binding motif B
F:464/Binding site: ATP (Lys) #status predicted
F:660/700/737/813/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent
F:686/790/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status expected
F:768/795/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent kinases)
F:894/900/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:1250/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 116; DB 1; Length 1480;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKECFDME 22
DB 817 GLEISEINEEDLKECFDME 838

RESULT 2

A:Accession: A39323

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Jun-1992 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A39323

R:Diamond: G.; Scanlin: T.F.; Zaslloff, M.A.; Bevins, C.L.

J. Biol. Chem. 266, 22761-22769, 1991

A:Title: A cross-species analysis of the cystic fibrosis transmembrane conductance regul

A:Reference number: A39323; PMID:92042228; PMID:1719001

A:Accession: A39323

A:Molecule type: mRNA

A:Residues: 1-1481 <DIA>

A:Cross-References: GB:M6128; NID:q163741; PIDN:AAA30772.1; PID:q163742

A:Note: the authors translated the codon GGA for residue 725 as Phe and AGA for residue

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;

F:81-102/Domain: transmembrane #status predicted <TM1>

F:118-138/Domain: transmembrane #status predicted <TM2>

F:195-215/Domain: transmembrane #status predicted <TM3>

F:221-241/Domain: transmembrane #status predicted <TM4>

F:308-328/Domain: transmembrane #status predicted <TM5>

F:331-350/Domain: transmembrane #status predicted <TM6>

F:440-621/Domain: ATP-binding cassette homology <ABC1>

F:457-464/Region: nucleotide-binding motif A (P-loop)

F:567-571/Region: nucleotide-binding motif B

F:589-830/Region: R domain

F:860-880/Domain: transmembrane #status predicted <TM7>

F:912-932/Domain: transmembrane #status predicted <TM8>

F:991-1011/Domain: transmembrane #status predicted <TM9>

F:1103-1123/Domain: transmembrane #status predicted <TM10>

F:1129-1150/Domain: transmembrane #status predicted <TM11>

F:1228-1420/Domain: ATP-binding cassette homology <ABC2>

F:1245-1252/Region: nucleotide-binding motif A (P-loop)

F:1367-1371/Region: nucleotide-binding motif B

F:463/Binding site: ATP (Lys) #status predicted

F:659/699/736/813/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-depende

F:685/790/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status expe

F:767/795/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent kinas

F:894/900/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:1251/Binding site: ATP (Lys) #status predicted

Query Match

Best Local Similarity 91.4%; Score 106; DB 1; Length 1481;

Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKECFDME 22

DB 817 GLEISEINEEDLKECFDME 838

RESULT 3

A:Accession: JG6139

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 28-May-1999

C:Accession: JG6139; E39323

R:Hart, P.; March, J.D.; Levesque, P.C.; Collier, M.L.; Geary, Y.; Horowitz, B.; Hume

Proc. Natl. Acad. Sci. U.S.A. 93, 6343-6348, 1996

A:Title: Cystic fibrosis gene encodes a cAMP-dependent chloride channel in heart.

A:Reference number: JG6139; PMID:96270540; PMID:8692817

A:Accession: JG6139

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1450 <HAR>

A:Cross-References: GB:U40227

R:Diamond: G.; Scanlin: T.F.; Zaslloff, M.A.; Bevins, C.L.

J. Biol. Chem. 266, 22761-22769, 1991

A:Title: A cross-species analysis of the cystic fibrosis transmembrane conductance re

A:Reference number: A39323; PMID:92042228; PMID:1719001

A:Accession: E39323

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 574-604, 'N', 606-646, 'I', 648-684, 'P', 686-700, 'S', 702-718, 'V', 720-746 <DIA>

A:Comment: This regulator plays a role in defecting intracellular processing.

C:Genetics:

A:Gene: cfr

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding casse

C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; transmembrane

F:411-592/Domain: ATP-binding cassette homology <ABC1>

F:428-435/Region: nucleotide-binding motif A (P-loop)

F:1197-1389/Domain: ATP-binding cassette homology <ABC2>

F:1214-1221/Region: nucleotide-binding motif A (P-loop)

Query Match

Best Local Similarity 88.8%; Score 103; DB 2; Length 1450;

Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKECFDME 22

DB 787 GLEISEINEEDLKECFDME 808

RESULT 4

A:Accession: S23756

C:Species: Xenopus laevis (African clawed frog)

C>Date: 05-Mar-1994 #sequence_revision 01-Sep-1995 #text_change 02-Feb-2001

C:Accession: S23756

R:Tucker, S.J.; Tannahill, D.; Higgins, C.F.

Hum. Mol. Genet. 1, 77-82, 1992

A:Title: Identification and developmental expression of the Xenopus laevis cystic fib

A:Reference number: S23756; PMID:93244789; PMID:1284470

A:Accession: S23756

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1485 <TUC>
A:Cross-references: EMBL:X65256; NID:964622; PIDN:CAA6348.1; PID:964623
C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette
C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein
F:442-623/Domain: ATP-binding cassette homology <ABC1>
F:459-466/Region: nucleotide-binding motif A (P-loop)
F:1230-1422/Domain: ATP-binding cassette homology <ABC2>
F:1247-1254/Region: nucleotide-binding motif A (P-loop)

Query Match 81.0%; Score 94; DB 2; Length 1485;
Best Local Similarity 81.0%; Pred. No. 8,6e-05;

Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 2 LEISEINEEDLKECFDDME 22
820 LEVSEINEEDLKECFDDTD 840

RESULT 5

Cystic fibrosis transmembrane conductance regulator - mouse (strain C57/BL/6J)

C:Species: Mus musculus domesticus (western European house mouse)

C:Date: 20-Mar-1992 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A39901; A42007

R:Title: Cloning the mouse homolog of the human cystic fibrosis transmembrane conductance

A:Reference number: A39901; MUID:91301683; PMID:1712752

A:Accession: A39901

A:Molecule type: mRNA

A:Residues: 1-1476 <TAT>

A:Cross-references: GB:M6298; NID:9192566; PIDN:AAA37417.1; PID:9192567

R:Kelley, K.A.; Stamm, S.; Kozak, C.A.

Genomics 13, 381-388, 1992

A:Title: Expression and chromosome localization of the murine cystic fibrosis transmembrane

A:Reference number: A42007; MUID:92307673; PMID:1377165

A:Accession: A42007

A:Molecule type: DNA

A:Residues: 465-528 <KEL>

A:Cross-references: GB:M64614

C:Genetics:

A:Gene: CFTR

A:Map position: 6

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;

F:81-102/Domain: transmembrane #status predicted <TM1>

F:118-138/Domain: transmembrane #status predicted <TM2>

F:195-215/Domain: transmembrane #status predicted <TM3>

F:221-241/Domain: transmembrane #status predicted <TM4>

F:308-328/Domain: transmembrane #status predicted <TM5>

F:331-350/Domain: transmembrane #status predicted <TM6>

F:441-622/Domain: transmembrane #status predicted <ABC1>

F:458-465/Region: nucleotide-binding motif A (P-loop)

F:568-572/Region: nucleotide-binding motif B

F:590-825/Region: R domain

F:855-875/Domain: transmembrane #status predicted <TM7>

F:907-927/Domain: transmembrane #status predicted <TM8>

F:986-1006/Domain: transmembrane #status predicted <TM9>

F:1098-1118/Domain: transmembrane #status predicted <TM10>

F:1124-1145/Domain: transmembrane #status predicted <TM11>

F:1223-1415/Domain: ATP-binding cassette homology <ABC2>

F:1240-1247/Region: nucleotide-binding motif A (P-loop)

F:1362-1366/Region: nucleotide-binding motif B

F:464/Binding site: ATP (Lys) #status predicted

F:660-698-732-808/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent

F:684-785/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experim

F:763-790/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent kinases)

F:889-895/Binding site: carboxylate (Asn) (covalent) #status predicted

F:1246/Binding site: ATP (Lys) #status predicted

Query Match 75.0%; Score 87; DB 1; Length 1476;

Best Local Similarity 80.0%; Pred. No. 0.00079;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 2 LEISEINEEDLKECFDDM 21
813 LNTSEINEEDLKECFDDV 832

RESULT 6

A40303

Cystic fibrosis transmembrane conductance regulator - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Apr-1992 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A40303; I78528

R:Yorifuji, T.; Lemna, W.K.; Ballard, C.F.; Rosenblom, C.L.; Rozmahel, R.; Plavsky,

Genomics 10, 547-550, 1991

A:Title: Molecular cloning and sequence analysis of the murine cDNA for the cystic fi

A:Reference number: A40303; MUID:91365359; PMID:1716243

A:Accession: A40303

A:Molecule type: mRNA

A:Residues: 1-1476 <YOR>

A:Cross-references: GB:M60493; NID:9192831; PIDN:AAA18903.1; PID:9192832

A:Experimental source: lung, strain BALB/cBy

R:Delany, S.J.; Rich, D.P.; Thomson, S.A.; Hargrave, M.R.; Lovelock, P.K.; Welsh, M.

Nature Genet. 4, 426-431, 1993

A:Title: Cystic fibrosis transmembrane conductance regulator splice variants are not

A:Reference number: I58115; MUID:94004974; PMID:7691356

A:Accession: I78528

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 549-571 <RES>

A:Cross-references: GB:S65942; NID:9430810; PIDN:AAB28391.1; PID:9430811

C:Genetics:

A:Gene: CFTR

A:Map position: 6

A:Introns: 560/2

A>Note: the list of introns is incomplete

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding case

C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein

F:81-102/Domain: transmembrane #status predicted <TM1>

F:118-138/Domain: transmembrane #status predicted <TM2>

F:195-215/Domain: transmembrane #status predicted <TM3>

F:221-241/Domain: transmembrane #status predicted <TM4>

F:308-328/Domain: transmembrane #status predicted <TM5>

F:331-350/Domain: transmembrane #status predicted <TM6>

F:441-622/Domain: transmembrane #status predicted <ABC1>

F:458-465/Region: nucleotide-binding motif A (P-loop)

F:568-572/Region: nucleotide-binding motif B

F:590-825/Region: R domain

F:855-875/Domain: transmembrane #status predicted <TM7>

F:907-927/Domain: transmembrane #status predicted <TM8>

F:986-1006/Domain: transmembrane #status predicted <TM9>

F:1098-1118/Domain: transmembrane #status predicted <TM10>

F:1124-1145/Domain: transmembrane #status predicted <TM11>

F:1223-1415/Domain: ATP-binding cassette homology <ABC2>

F:1240-1247/Region: nucleotide-binding motif A (P-loop)

F:1362-1366/Region: nucleotide-binding motif B

F:464/Binding site: ATP (Lys) #status predicted

F:660-698-732-808/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-depende

F:684-785/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status exper

F:763-790/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent kins

F:889-895/Binding site: carboxylate (Asn) (covalent) #status predicted

F:1246/Binding site: ATP (Lys) #status predicted

Query Match 75.0%; Score 87; DB 1; Length 1476;
Best Local Similarity 80.0%; Pred. No. 0.00079;

Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 2 LEISEINEEDLKECFDDM 21
813 LNTSEINEEDLKECFDDV 832

RESULT 7

A59322
 cystic fibrosis transmembrane conductance regulator homolog - spiny dogfish
 C:Species: *Squalus acanthias* (spiny dogfish)
 C:Date: 19-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 20-Aug-1999
 C:Accession: A59322
 R:Marshall, J.; Martin, K.A.; Piccioletto, M.; Hockfield, S.; Nairn, A.C.; Kaczmarek, L.K.
 J. Biol. Chem. 266, 22749-22754, 1991
 A:Title: Identification and localization of a dogfish homolog of human cystic fibrosis r
 A:Reference number: A59322; MUID:92042226; PMID:1718999
 A:Accession: A59322
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1492 <MAR>
 A:Cross-references: GB:M83785; GB:M76974; NID:g213869; PIDN:AAA9616.1; PID:g213870
 A:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette
 C:Keywords: ATP; duplication; glycoprotein; membrane protein; nucleotide binding; P-loop
 F:442-623/Domain: ATP-binding cassette homology <ABC1>
 F:459-467/Region: nucleotide-binding motif A (P-loop)
 F:569-573/Region: nucleotide-binding motif B
 F:1237-1429/Domain: ATP-binding cassette homology <ABC2>
 F:1254-1362/Region: nucleotide-binding motif A (P-loop)
 F:1376-1380/Region: nucleotide-binding motif B
 F:465/Binding site: ATP (Lys) #status predicted
 F:1260/Binding site: ATP (Lys) #status predicted

Query Match - 75.0%; Score 87; DB 2; Length 1492;
 Best Local Similarity 85.0%; Pred. No. 0.0008;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EISEINEEDLKECFDME 22
 |||||

Db 828 EISEINEEDLKECFADDEE 847

RESULT 8

A32916
 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Vibrio harveyi
 C:Species: *Vibrio harveyi*
 C:Date: 08-Dec-1989 #sequence_revision 02-Jun-2000 #text_change 03-Jun-2002
 C:Accession: A32916; B23866; A35081
 R:Johnston, T.C.; Hruska, K.S.; Adams, L.F.
 Biochem. Biophys. Res. Commun. 163, 93-101, 1989
 A:Title: The nucleotide sequence of the luxE gene of *Vibrio harveyi* and a comparison of
 A:Reference number: A32916; MUID:89374304; PMID:2775296
 A:Accession: A32916
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-378 <JOH1>
 A:Cross-references: GB:M28815; NID:g155209; PIDN:AAA27531.1; PID:g155211
 R:Johnston, T.C.; Thompson, R.B.; Baldwin, T.O.
 J. Biol. Chem. 261, 4805-4811, 1986
 A:Title: Nucleotide sequence of the luxB gene of *Vibrio harveyi* and the complete amino a
 A:Reference number: A23866; MUID:8618191; PMID:3514602
 A:Accession: B23866
 A:Molecule type: DNA
 A:Residues: 1-1492 <JOH2>
 A:Cross-references: GB:M10961; NID:g155174; PIDN:AAA8687.1; PID:g1197015
 A:Note: an incorrect initiation codon was used
 R:Swartzman, E.; Miyamoto, C.; Graham, A.; Weighen, E.
 J. Biol. Chem. 265, 3513-3517, 1990
 A:Title: Delineation of the transcriptional boundaries of the lux operon of *Vibrio harveyi*
 A:Reference number: A35081; MUID:90154014; PMID:2303459
 A:Accession: A35081
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 370-378 <SWA>
 A:Cross-references: GB:M27139; NID:g155225
 A:Note: this translation is not annotated in Genbank entry VIBLUXGH, release 113.0
 C:Genetics:
 A:Gene: luxE
 C:Keywords: acid-thiol ligase

F:362/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 49.1%; Score 57; DB 2; Length 378;
 Best Local Similarity 45.0%; Pred. No. 2.6;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 EISEINEEDLKECFDME 22
 |||||

Db 265 QINDTNEEDLKECFDME 284

RESULT 9

H89900
 translation initiation factor IF-2 [imported] - *Staphylococcus aureus* (strain N315)
 C:Species: *Staphylococcus aureus*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 31-Dec-2001
 C:Accession: H89900
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
 ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: H89900
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-705 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701069; PIDN:BA842364.1; GSPDB:GN00149
 A:Experimental source: strain N315
 A:Genetics:
 A:Gene: infB
 C:Superfamily: translation initiation factor IF-2; translation elongation factor Tu h

Query Match 44.0%; Score 51; DB 2; Length 705;
 Best Local Similarity 50.0%; Pred. No. 33;
 Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 1 GLEISEE--INEEDLKECFDME 22
 |||||

Db 178 GVEVEEVEINEEDLSTYFDEKD 201

RESULT 10

S67268
 hypothetical protein YOR356w - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein O6629
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
 C:Accession: S67268
 R:Delius, H.; Hebling, U.; Hofmann, B.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67261
 A:Accession: S67268
 A:Molecule type: DNA
 A:Residues: 1-631
 A:Cross-references: EMBL:275264; NID:g1420773; PID:e252180; PID:g1420774; GSPDB:GN000
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: MIPS:YOR356w
 A:Cross-references: SGD:S0005883
 A:Map position: 15R

Query Match 43.1%; Score 50; DB 2; Length 631;
 Best Local Similarity 47.4%; Pred. No. 41;
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKECFD 19
 |||||

Db 417 GLPYLEVEDEDAKMAFD 435

RESULT 11

A28664

RESULT 13
 A64603
 coproporphyrinogen oxidase (EC 1.3.3.3) III, oxygen-independent HP0665 - *Helicobacter pylori*
 C:Species: *Helicobacter pylori*
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 20-Sep-1999
 C:Accession: A64603
 R:Contig: J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khairak, H.G.; Glodek, A.; McMenne-
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: A64603

RESULT 15
0080011

Probable calmodulin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 23-Mar-2001
C:Accession: G85041
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85041
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1154 <STO>
A:Cross-references: GB:NC_001268; NID:97270199; PIDN:CAB77814.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g03290
A:Map position: 4
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 41.4%; Score 48; DB 2; Length 154;
Best local similarity 50.0%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 4; Indels 2; Gaps 1;
QY 2 LEISEINEEDLKECF--FD 19
:|:|:|:|:|:|:|:|:|
Db 71 VEDEDEVGEEDMKKAFNVFD 90

Search completed: July 16, 2003, 14:03:53
Job time : 41 secs